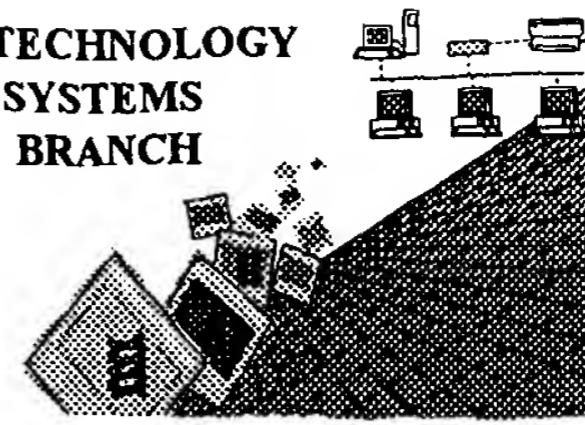


al-muw

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/697,863
Source: 1600
Date Processed by STIC: 11/13/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/697,863

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|--|--|
| 1 | ____ Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 | ____ Wrapped Aminos | The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 | ____ Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 | ____ Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 | ____ Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 | ____ Variable Length | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 7 | ____ PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 8 | ____ Skipped Sequences
(OLD RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 | ____ Skipped Sequences
(NEW RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
<210> sequence id number
<400> sequence id number
000 |
| 10 | ____ Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 11 | ____ Use of <213>Organism
(NEW RULES) | Sequence(s) ____ are missing this mandatory field or its response. |
| 12 | ____ Use of <220>Feature
(NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 | ____ PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. |

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/697,863¹

DATE: 11/13/2000
TIME: 17:30:41

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\11132000\I697863.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
5 <120> TITLE OF INVENTION: CD40-INTERACTING AND TRAF-INTERACTING PROTEINS
7 <130> FILE REFERENCE: V7/002-V018
9 <140> CURRENT APPLICATION NUMBER: US/09/697,863
10 <141> CURRENT FILING DATE: 2000-10-27
12 <150> PRIOR APPLICATION NUMBER: 98201392.2
13 <151> PRIOR FILING DATE: 1998-04-29
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
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21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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25 <221> NAME/KEY: CDS
26 <222> LOCATION: (20)..(1108)
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34 Glu Ala Ala Glu Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu
35 15 20 25
37 ctg tgt gtg gag ttt gcc tcc gtc gca agc tgc gat gcc gca gtg gct 148
38 Leu Cys Val Glu Phe Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala
39 30 35 40
41 cag tgc ttc ctg gcc gag aac gac tgg gag atg gaa agg gct ctg aac 196
42 Gln Cys Phe Leu Ala Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn
43 45 50 55
45 tcc tac ttc gag cct ccg gtg gag gac agc gcc ttg gaa cgc cga cct 244
46 Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro
47 60 65 70 75
49 gaa acc atc tct gag ccc aag acc tat gtt gac cta acc aat gaa gaa 292
50 Glu Thr Ile Ser Glu Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu
51 80 85 90
53 aca act gat tcc acc aci tct aaa atc agc cca tct gaa gat act cag 340
54 Thr Thr Asp Ser Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln
55 95 100 105
57 caa gaa aat ggc agc atg ttc tct att acc tgg aat att gat gga 388
58 Gln Glu Asn Gly Ser Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly
59 110 115 120
61 tta gat cta aac aat ctg tca gag agg gct cga ggg gtg tgt tcc tac 436
62 Leu Asp Leu Asn Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr
63 125 130 135
65 tta gct ttg tac agc cca gat gtg ata ttt cta cag gaa gtt att ccc 484
66 Leu Ala Leu Tyr Ser Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro
67 140 145 150 155

MP 23

rel P.S. prob

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/697,863

DATE: 11/13/2000
TIME: 17:30:41

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Output Set: N:\CRF3\11132000\I697863.raw

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74 Thr Gly His Glu Glu Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser	
75 175 180 185	
77 aya gtg aaa tta aaa agc caa gag att att cct ttt cca agt acc aaa	628
78 Arg Val Lys Leu Lys Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys	
79 190 195 200	
81 atg atg aga aac ctt tta tgt gtg cat gtg aat gtg tca gga aat gag	676
82 Met Met Arg Asn Leu Leu Cys Val His Val Asn Val Ser Gly Asn Glu	
83 205 210 215	
85 ctt tgc ctt atg aca tcc cat ttg gag ayc acc aya ggg cat gct gcg	724
86 Leu Cys Leu Met Thr Ser His Leu Glu Ser Thr Arg Gly His Ala Ala	
87 220 225 230 235	
89 gaa cga atg aat cag tta aaa atg gtt tta aag aaa atg caa qag gct	772
90 Glu Arg Met Asn Gln Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala	
91 240 245 250	
93 cca qag tca gct aca gtt ata ttt gca gga gat aca aat cta aqg gat	820
94 Pro Glu Ser Ala Thr Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp	
95 255 260 265	
97 cga gag gtt acc aga tgt ggt ggt tta ccc aac aac att gtg gat gtc	868
98 Arg Glu Val Thr Arg Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val	
99 270 275 280	
101 tgg gag ttt ttg ggc aaa cct aaa cat tgc caq tat aca tgg gat aca	916
102 Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr	
103 285 290 295	
105 caa atg aac tct aat ctt gga ata act gct gct tgt aaa ctt cgt ttt	964
106 Gln Met Asn Ser Asn Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe	
107 300 305 310 315	
109 gat cga ata ttt ttc aga qca qca gca gaa gag gga cac att att ccc	1012
110 Asp Arg Ile Phe Phe Arg Ala Ala Glu Glu Gly His Ile Ile Pro	
111 320 325 330	
113 cga agt ttg gac ctt ctt gga tta gaa aaa ctg gac tgt ggt aga ttt	1060
114 Arg Ser Leu Asp Leu Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe	
115 335 340 345	
117 cct agt gat cac tgg ggt ctt ctg tgc aac tta gat ata ata ttg taa	1108
118 Pro Ser Asp His Trp Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu	
119 350 355 360	
121 aatgttttc aagtgtgggt ttgcctgaa ttgttgcaaa tacaatttcc accttctgga	1168
123 aaggtaggtt tgctgtggag gaaataatgt actagatcat tgtcacagaa aaaccaacta	1228
125 tgatttatgg ttgtgttttc agaattcaac attaaagatt aatgtttatt taaaacgaa	1288
127 cattcctgca ttcaaggatgt gagggcattt aaaaaagg gcacaaagcc tgtcagagtt	1348
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133 agaaaacata agagattt gaggcttgg gactggatcc tttatttcat aagttcagat	1528
135 catcttaaat gaaaatgcca tgattatctg cagttaaat gatgacagct attctacatc	1588
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? see item 10 on
Error summary
sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/697,863

DATE: 11/13/2000
TIME: 17:30:41.

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\11132000\I697863.raw

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 163 35 40 45
 165 Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
 166 50 55 60
 168 Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu
 169 65 70 75 80
 171 Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr
 172 85 90 95
 174 Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser
 175 100 105 110
 177 Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn
 178 115 120 125
 180 Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser
 181 130 135 140
 183 Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr
 184 145 150 155 160
 186 Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile Thr Gly His Glu Glu
 187 165 170 175
 189 Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser Arg Val Lys Leu Lys
 190 180 185 190
 192 Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys Met Met Arg Asn Leu
 193 195 200 205
 195 Leu Cys Val His Val Asn Val Ser Gly Asn Glu Leu Cys Leu Met Thr
 196 210 215 220
 198 Ser His Leu Glu Ser Thr Arg Gly His Ala Ala Glu Arg Met Asn Gln
 199 225 230 235 240
 201 Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala Pro Glu Ser Ala Thr
 202 245 250 255
 204 Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp Arg Glu Val Thr Arg
 205 260 265 270
 207 Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val Trp Glu Phe Leu Gly
 208 275 280 285
 210 Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr Gln Met Asn Ser Asn
 211 290 295 300
 213 Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe Asp Arg Ile Phe Phe
 214 305 310 315 320

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/697,863

DATE: 11/13/2000
TIME: 17:30:41

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\11132000\I697863.raw

216 Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro Arg Ser Leu Asp Leu
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222 Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu
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228 <211> LENGTH: 1312
229 <212> TYPE: DNA
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241 q atg gca tct ggc aqc agt tcc qat gca gca gca gca gca gca 169
242 Met Ala Ser Gly Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro Ala
243 1 5 10 15
245 qgg cgg qcg tcg qca ccc qaa gca qca caq qcg qag qac cgg 217
246 Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp Arg
247 20 25 30
249 gtg aag agg cgg cgg ctt cag tgc ctg ggc ttt qcg ttg gtg ggg gga 265
250 Val Lys Arg Arg Arg Leu Gln Cys Leu Gly Phe Ala Leu Val Gly Gly
251 35 40 45
253 tgc gac ccc acg atg gtc ccc aqc gtc ctg cgg gag aac gac tgg cag 313
254 Cys Asp Pro Thr Met Val Pro Ser Val Leu Arg Gln Asn Asp Trp Gln
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258 Thr Gln Lys Ala Leu Ser Ala Tyr Phe Glu Leu Pro Glu Asn Asp Gln
259 65 70 75 80
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263 85 90 95
265 gat cta acc aac gag gat gca aat gat aca acc att tta gaa gcc agt 457
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271 115 120 125
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275 130 135 140
277 ggg gtg tgt tcc tgc cta gct ttg tat agt cca gat gtg gta ttt cta 601
278 Gly Val Cys Ser Cys Leu Ala Leu Tyr Ser Pro Asp Val Val Phe Leu
279 145 150 155 160
281 cag gaa gtt atc ccc cca tac tgt gcc tac cta aag aag aga gca gcc 649
282 Gln Glu Val Ile Pro Pro Tyr Cys Ala Tyr Leu Lys Lys Arg Ala Ala
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RAW SEQUENCE LISTING DATE: 11/13/2000
PATENT APPLICATION: US/09/697,863 TIME: 17:30:41

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\11132000\I697863.raw

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 286 Ser Tyr Thr Ile Ile Thr Gly Asn Glu Glu Gly Tyr Phe Thr Ala Ile
 287 180 185 190
 289 cta ttg aag aaa gga aga gtg aaa ttt aaa agt cag gag att att cct 745
 290 Leu Leu Lys Lys Gly Arg Val Lys Phe Lys Ser Gln Glu Ile Ile Pro
 291 195 200 205
 293 ttt cca aat acc aaa atg atg aga aac ctg cta tgc gta aat gtg aqt 793
 294 Phe Pro Asn Thr Lys Met Met Arg Asn Leu Leu Cys Val Asn Val Ser
 295 210 215 220
 297 ttg ggt gga aat gaa ttt tgc ctt atg aca tcc cat ttg gag agc acc 841
 298 Leu Gly Gly Asn Glu Phe Cys Leu Met Thr Ser His Leu Glu Ser Thr
 299 225 230 235 240
 301 aga gaa cat tct gcg gaa cga ata aqa caa tta aaa act gtt ctt gga 889
 302 Arg Glu His Ser Ala Glu Arg Ile Arg Gln Leu Lys Thr Val Leu Gly
 303 245 250 255
 305 aaa atg caa gaa gat cca gat tca acc acg gtt ata ttt gca gga qat 937
 306 Lys Met Gln Glu Ala Pro Asp Ser Thr Thr Val Ile Phe Ala Gly Asp
 307 260 265 270
 309 aca aat tta aga gat caa gaa gtt atc aaa tgt ggt ggt tta cct gac 985
 310 Thr Asn Leu Arg Asp Gln Glu Val Ile Lys Cys Gly Leu Pro Asp
 311 275 280 285
 313 aac gtt ttt gat gcc tgg gaa ttt tta ggc aaa cct aaa cat tgc cag 1033
 314 Asn Val Phe Asp Ala Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln
 315 290 295 300
 317 tat aca tgg gat acg aaa gca aat aac aac ctc agg atc cct gct gct 1081
 318 Tyr Thr Trp Asp Thr Lys Ala Asn Asn Asn Leu Arg Ile Pro Ala Ala
 319 305 310 315 320
 321 tat aag cat cgt ttt gat cga ata ttt ttc aga gca gaa gag ggg cac 1129
 322 Tyr Lys His Arg Phe Asp Arg Ile Phe Phe Arg Ala Glu Glu Gly His
 323 325 330 335
 325 ctt att cct caa agt tta gac ctt gtt ggg ttg gaa aaa ctg gac tgt 1177
 326 Leu Ile Pro Gln Ser Leu Asp Leu Val Gly Leu Glu Lys Ieu Asp Cys
 327 340 345 350
 329 ggt aga ttt ccg agt gat cac tgg ggg ctc ttg tgc acc ttg aat gta 1225
 330 Gly Arg Phe Pro Ser Asp His Trp Gly Leu Leu Cys Thr Leu Asn Val
 331 355 360 365
 333 gta ttg tga aaagcttccc acttgagct ttacacgtt gtttagcacta 1274
 334 Val Leu
 335 370
 337 gttctgaatt ttttgttagtc tcaaaccttcc aggacatc 1312
 340 <210> SEQ ID NO: 4
 341 <211> LENGTH: 370
 342 <212> TYPE: PRT
 343 <213> ORGANISM: Mus musculus
 345 <400> SEQUENCE: 4
 346 Met Ala Ser Gly Ser Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro Ala
 347 1 5 10 15
 349 Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp Arg
 350 20 25 30

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/697,863

DATE: 11/13/2000
TIME: 17:30:42

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\11132000\I697863.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:137 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:137 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:145 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:536 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:536 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:537 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:548 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:549 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:630 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:630 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:630 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:630 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:630 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:639 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:639 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:639 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:639 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6